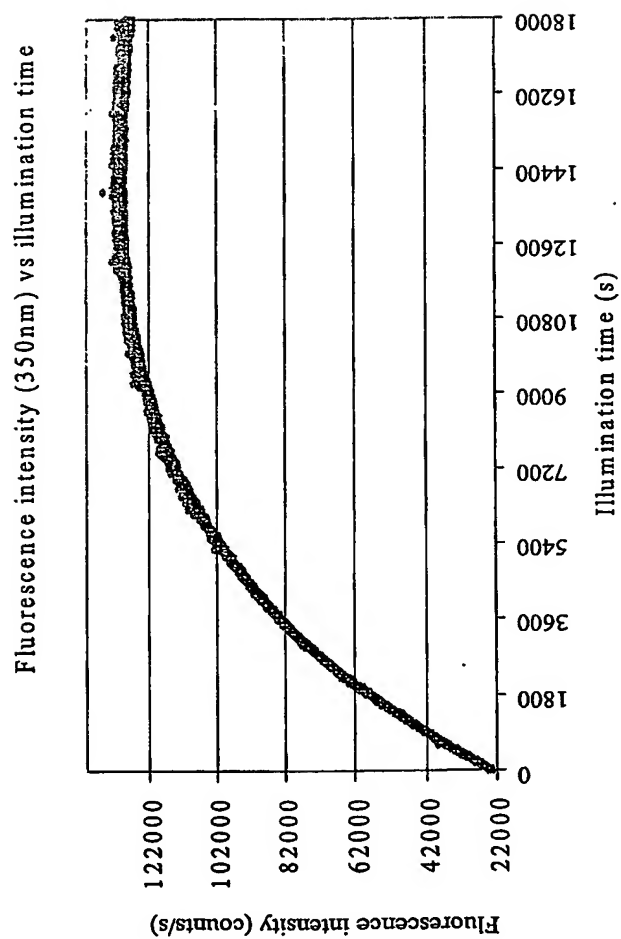


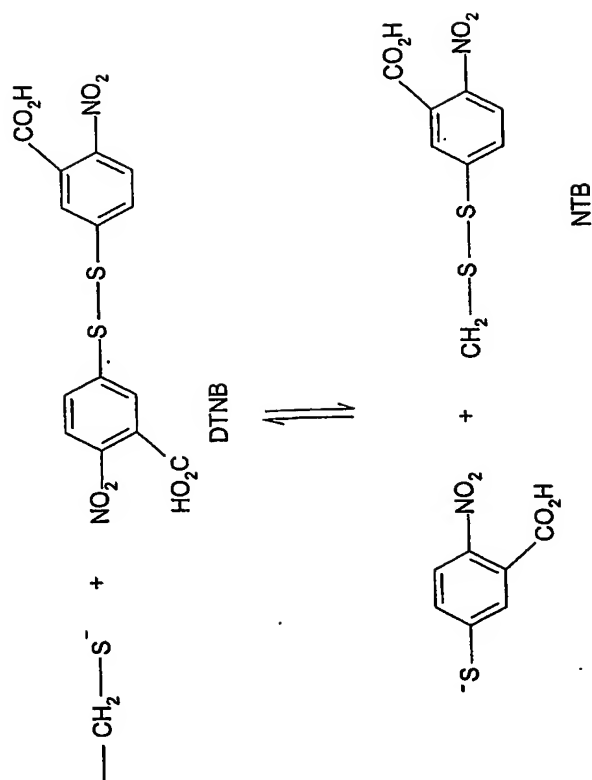
1/20

Figure 1



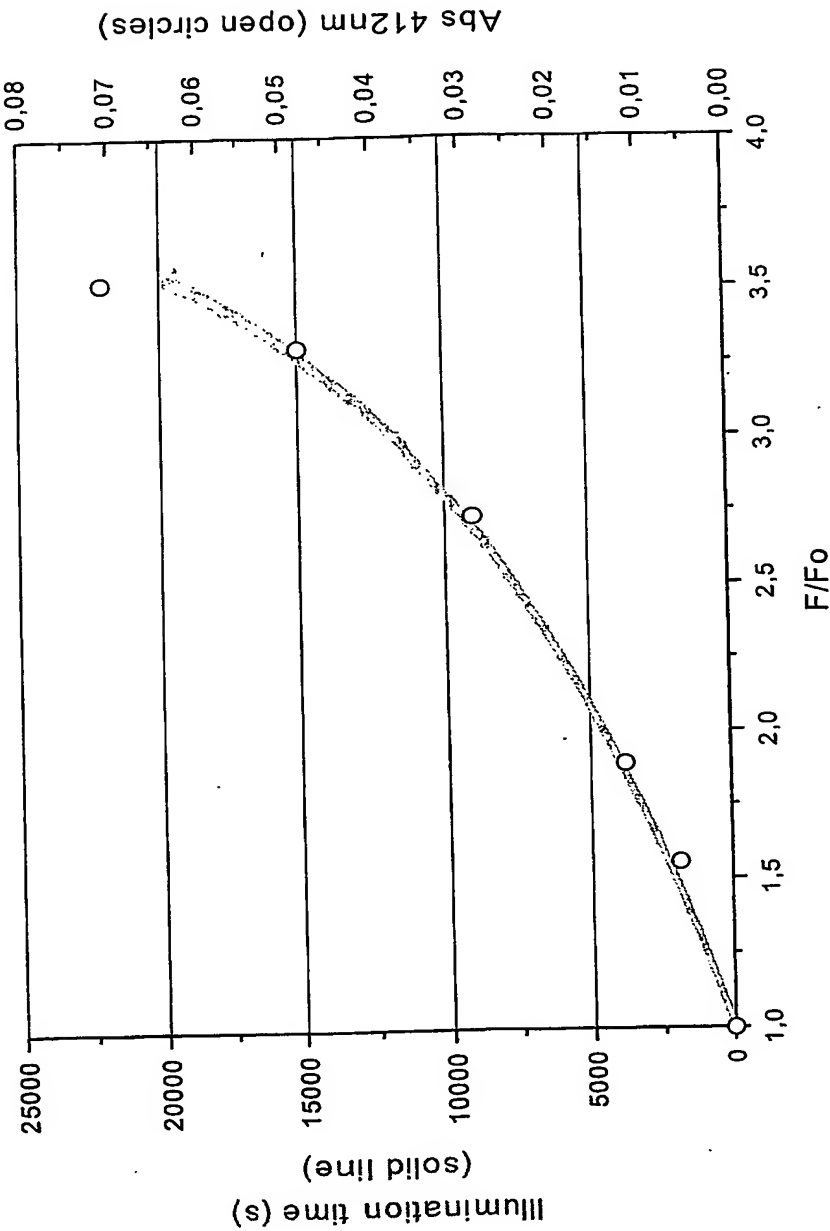
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Figure 2



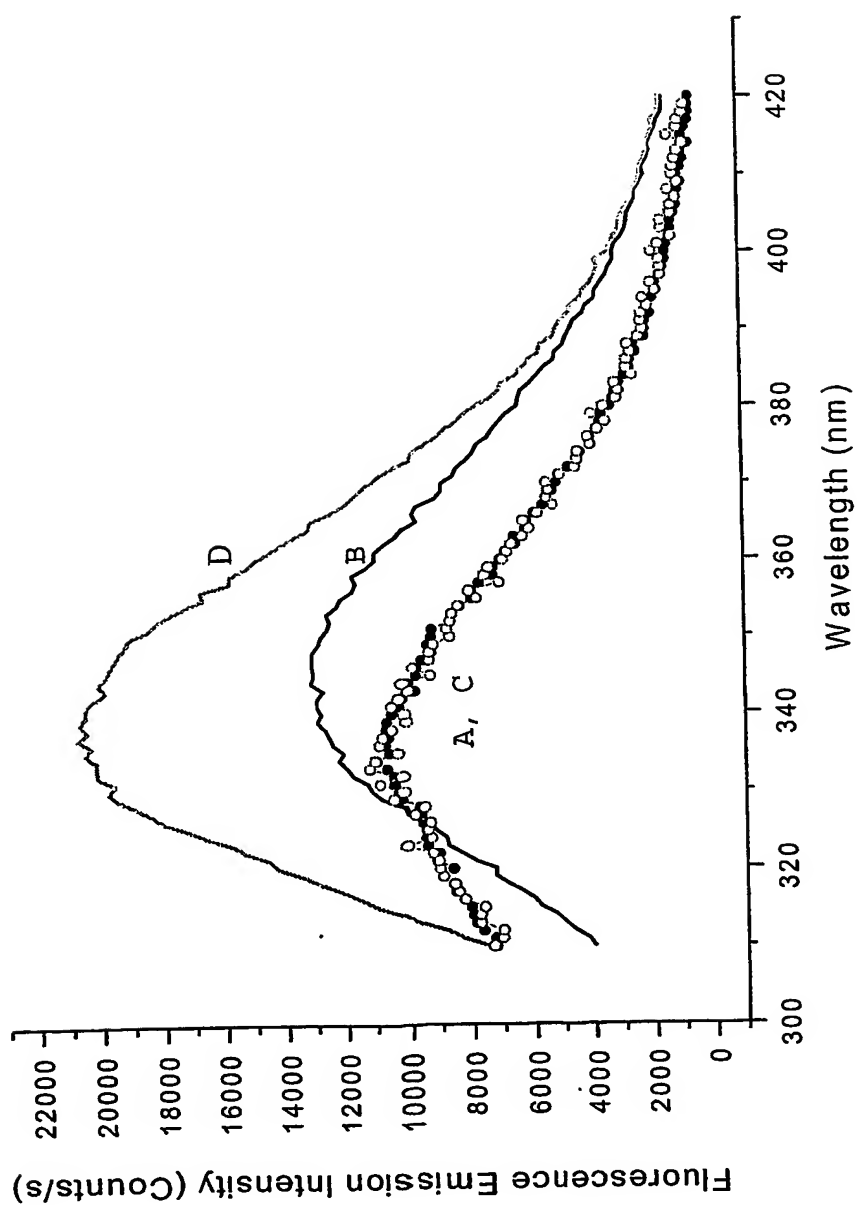
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Figure 3



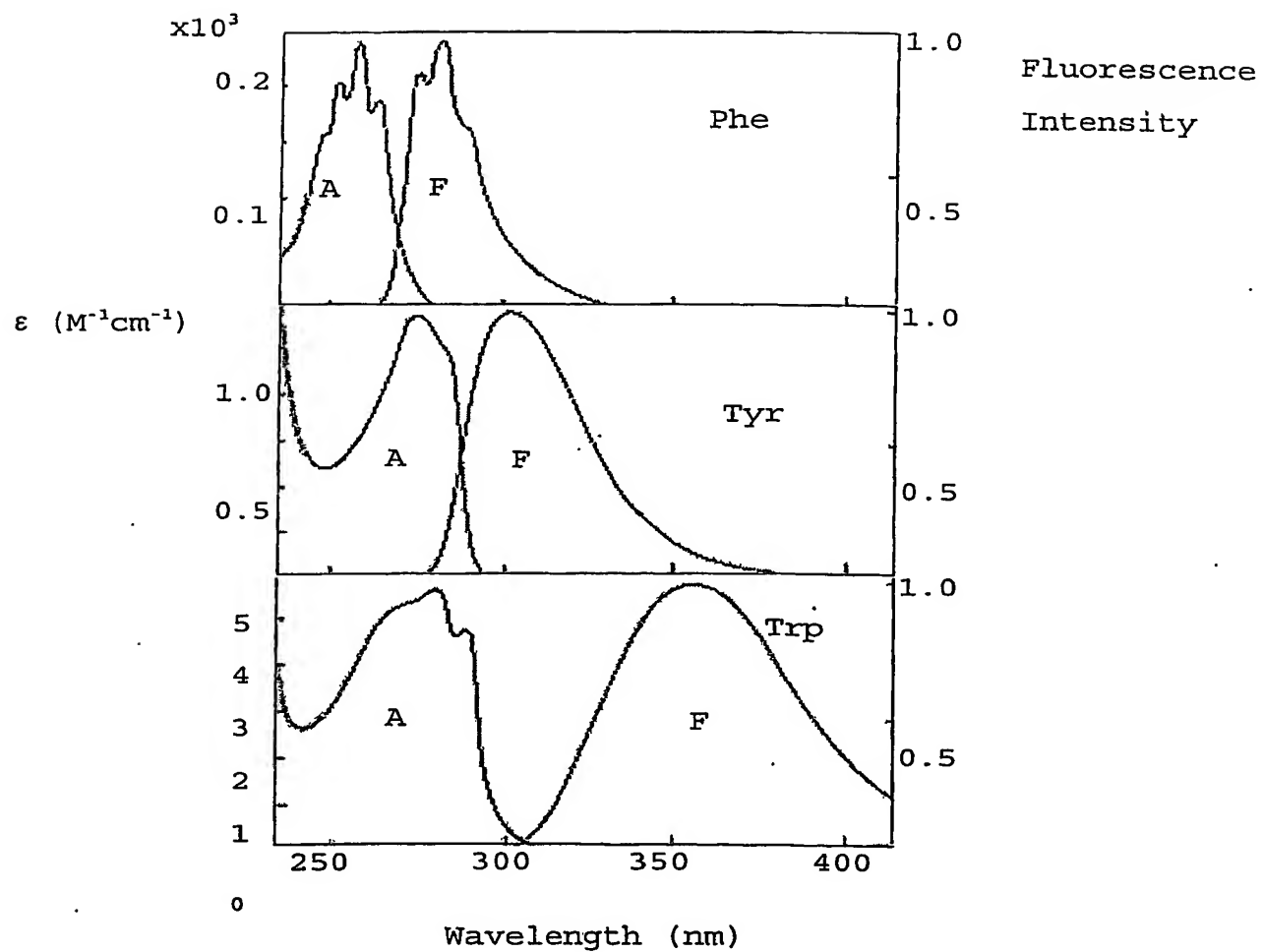
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Figure 4



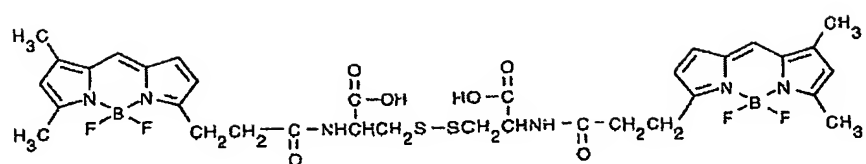
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Figure 5



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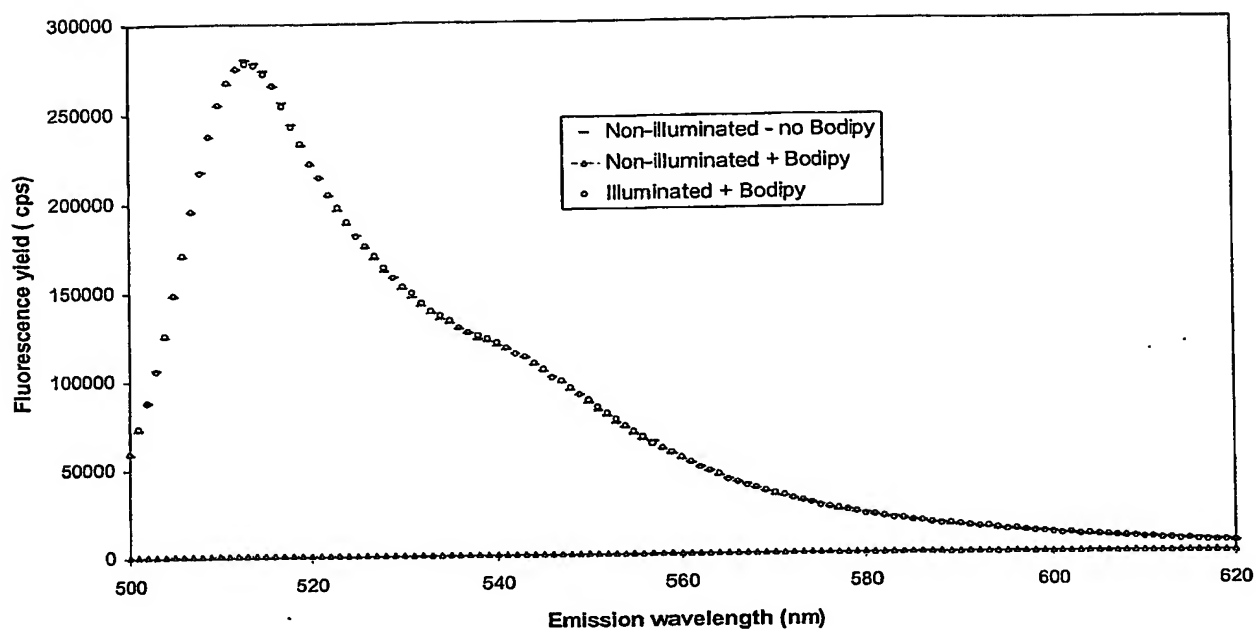
Figure 6



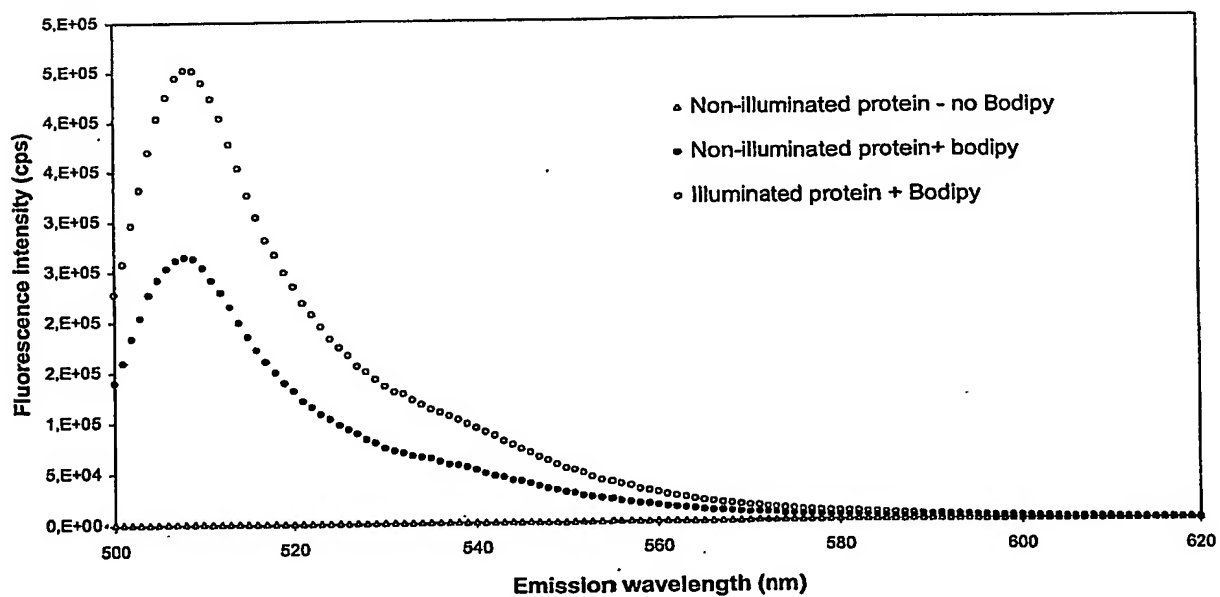
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Figure 7

A

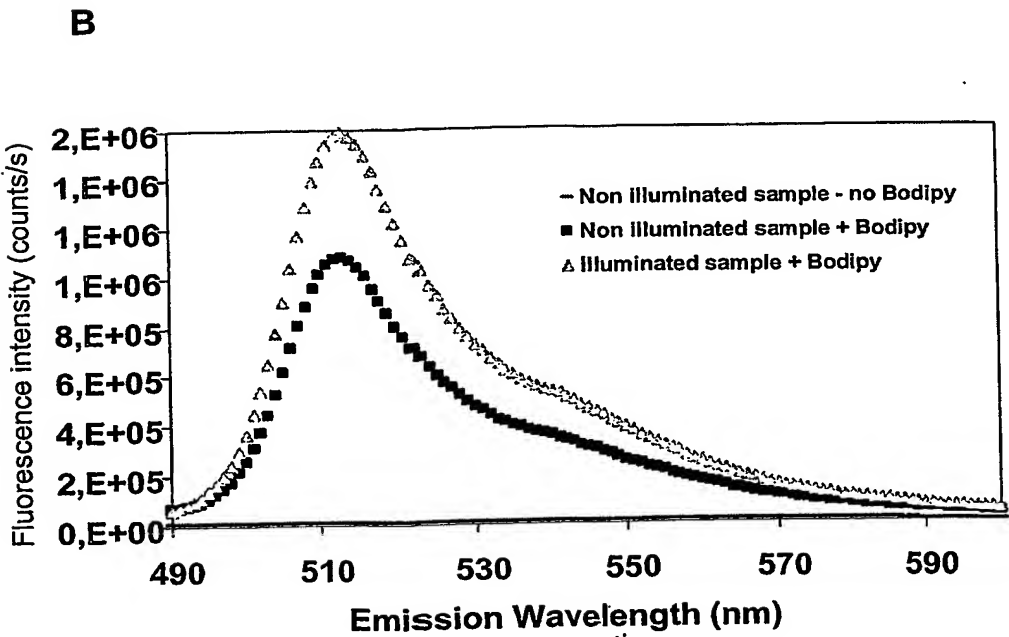
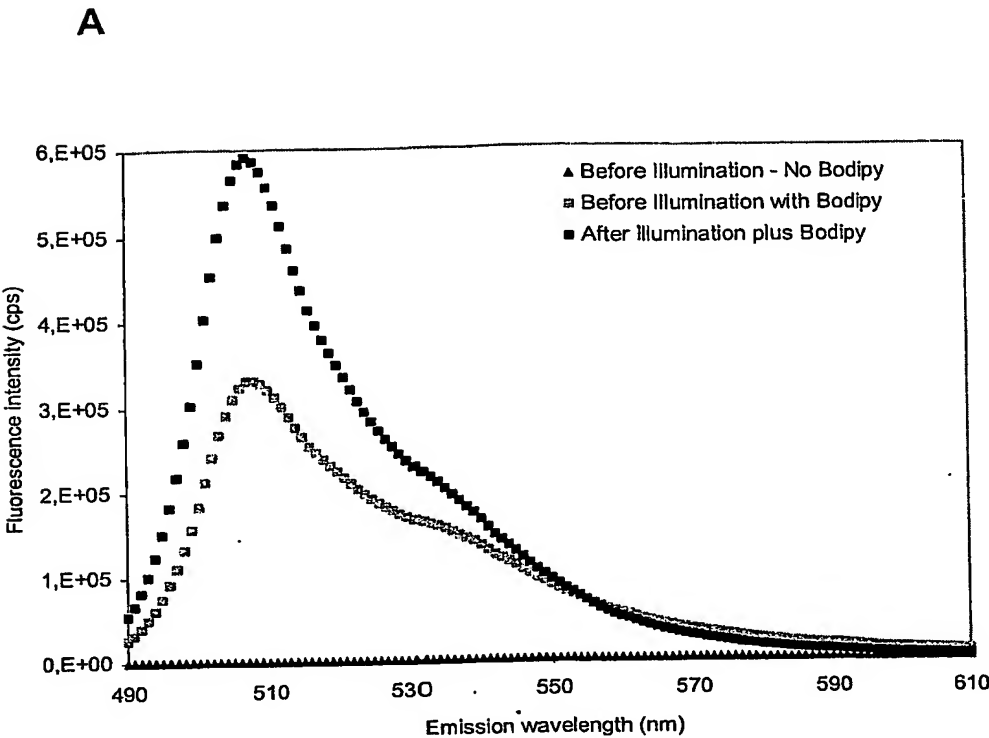


B



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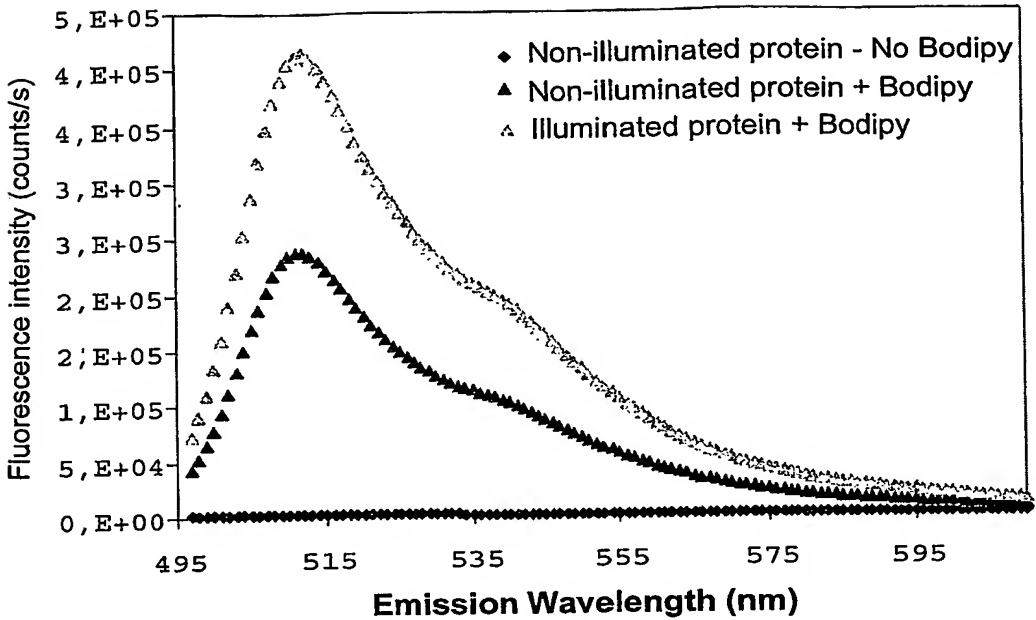
Figure 8



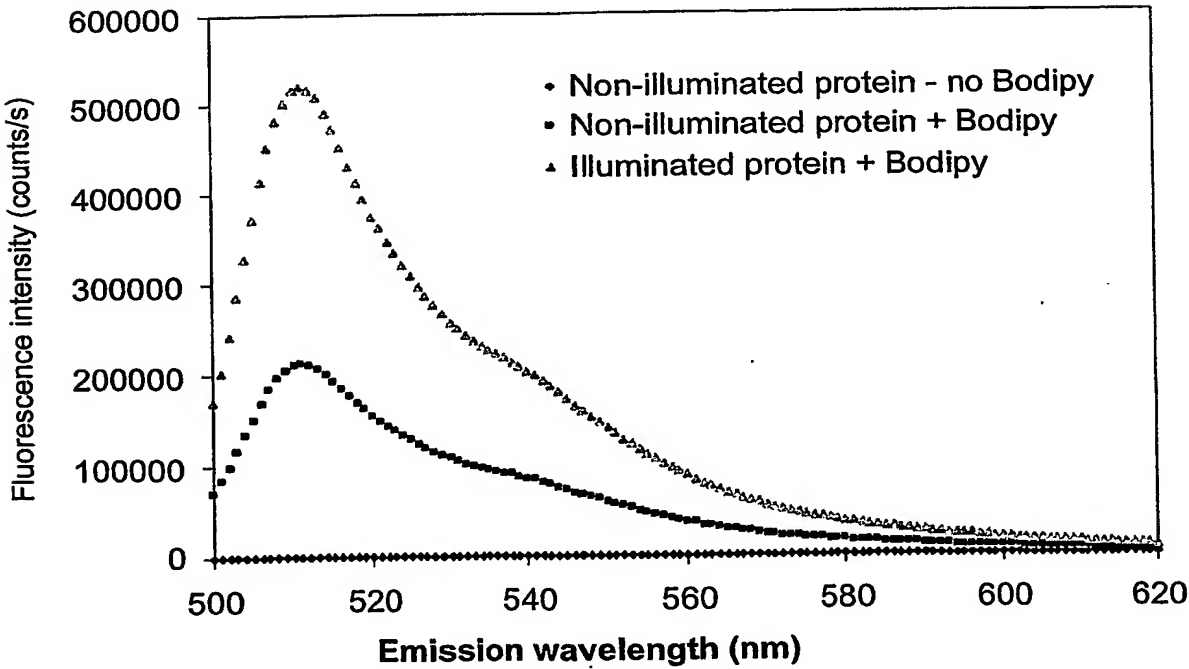


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C



D



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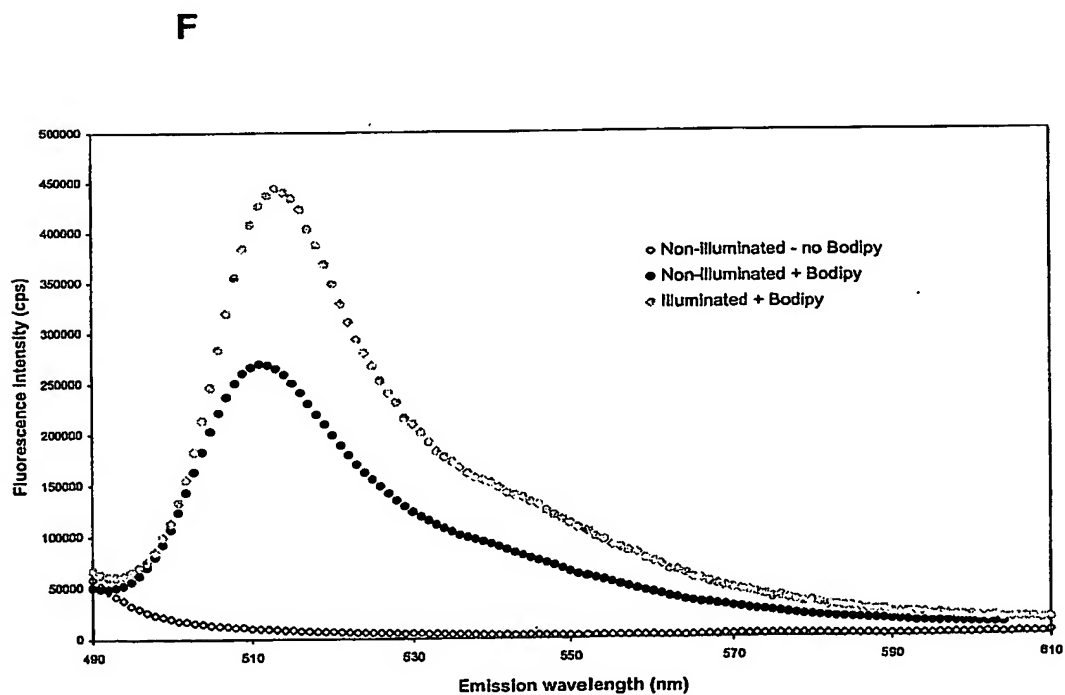
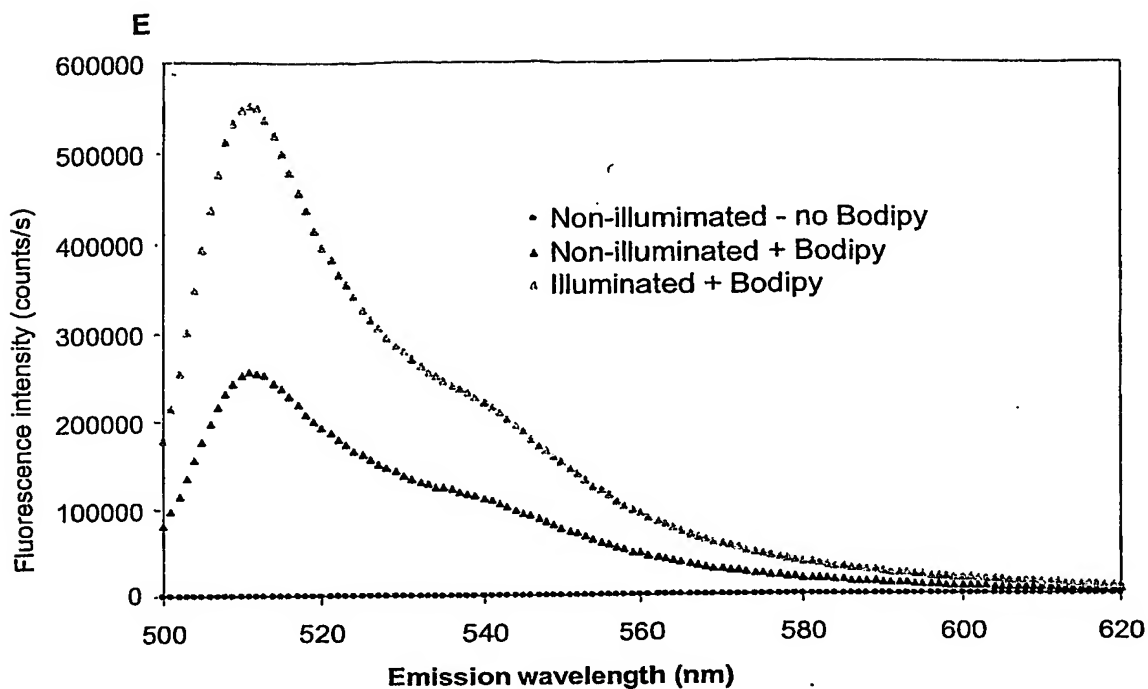


Figure 9

8 Ångström neighbourhood

The "score" is the result of :  $f(\text{subset})/f(\text{protein})$

Therefore: "scores" > 1 means that residue/group is overrepresented  
"scores" < 1 means that residue/group is underrepresented

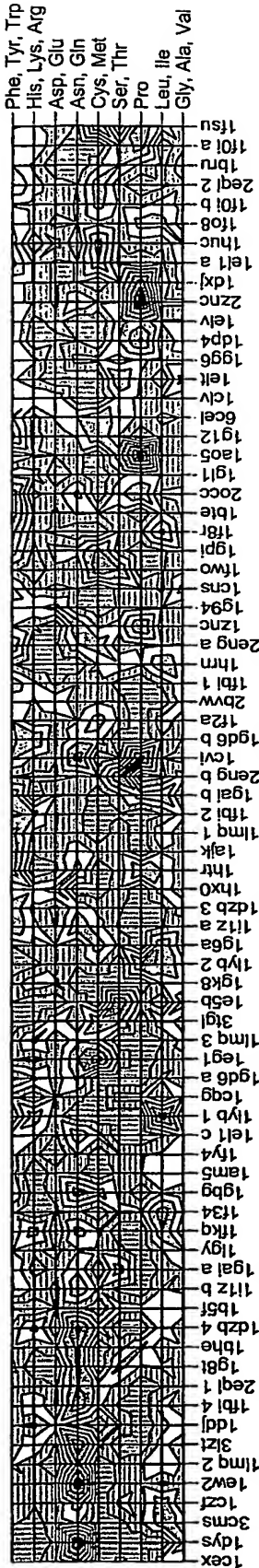
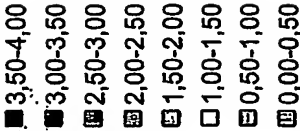




Figure 11

8 Ångström neighbourhood

The triad of cutinase compared to IGG1 triads A)

The "score" is the result of :  $f(\text{subset})/f(\text{protein})$

Therefore: "scores" > 1 means that residue/group is overrepresented

"scores" < 1 means that residue/group is underrepresented

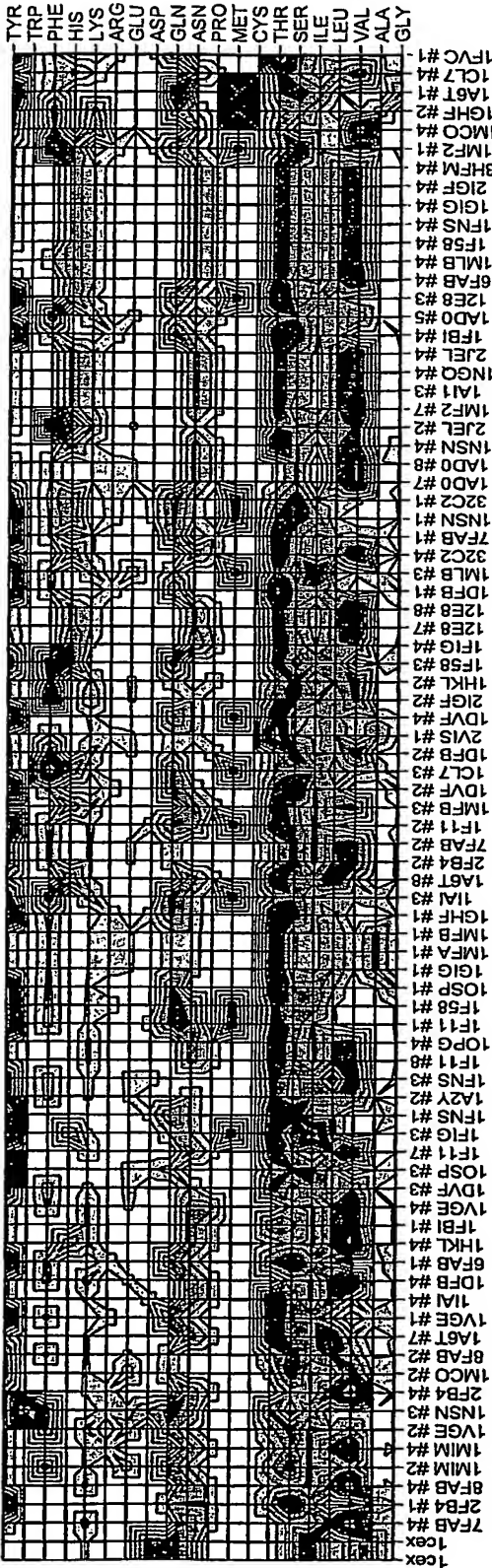
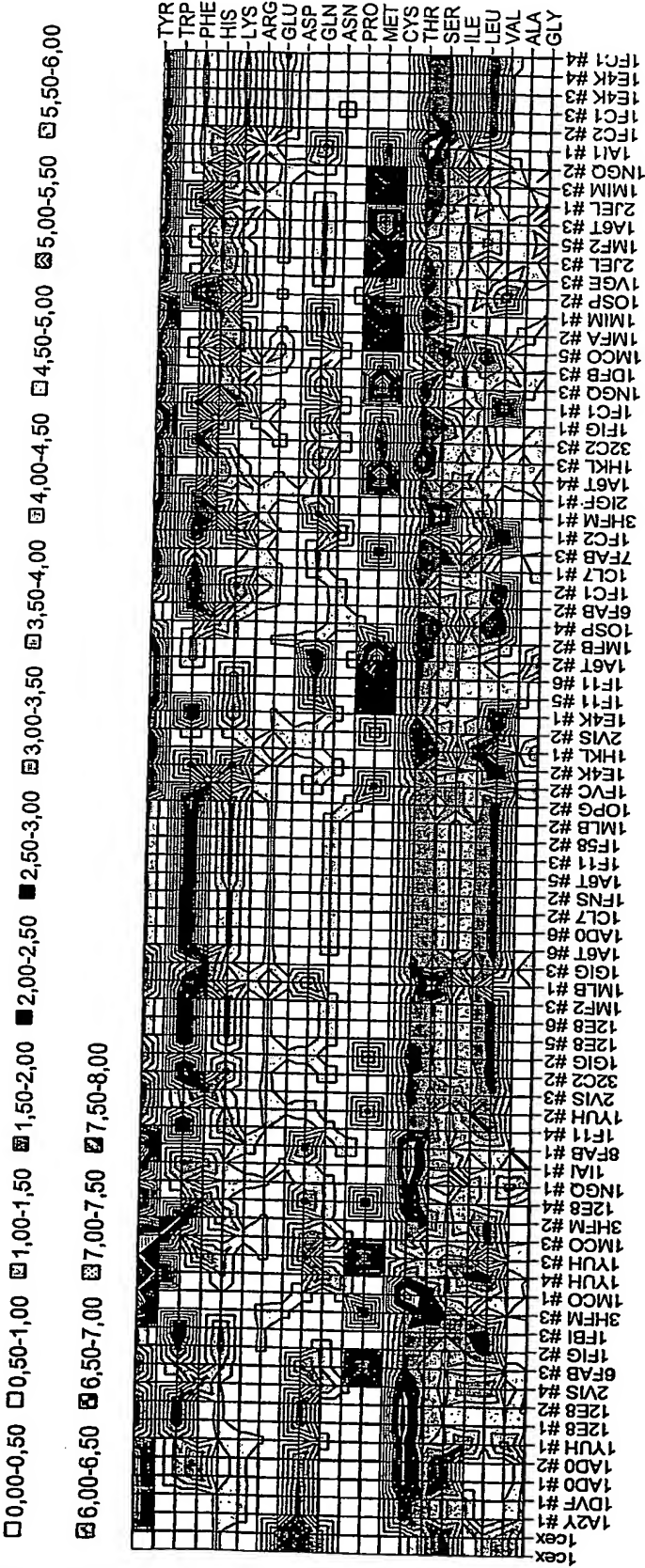


Figure 12

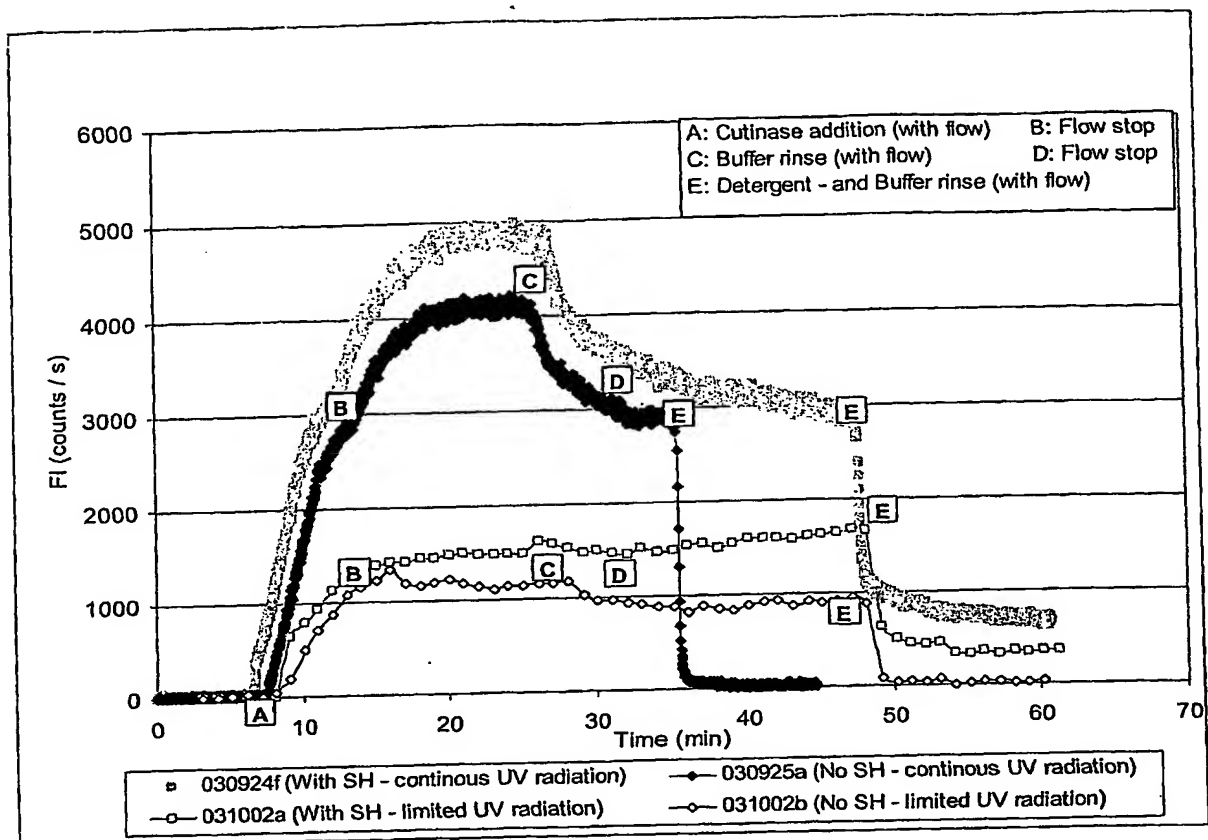
8 Ångström neighbourhood  
The triad of cutinase compared to IGG1 triads B)  
The "score" is the result of :  $f(\text{subset})/f(\text{protein})$

Therefore: "scores" > 1 means that residue/group is overrepresented  
"scores" < 1 means that residue/group is underrepresented



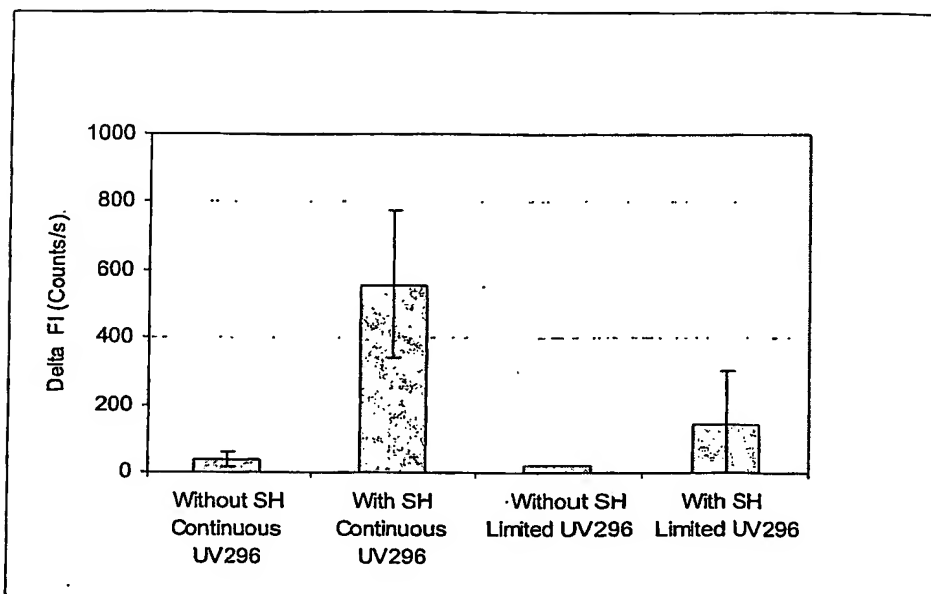
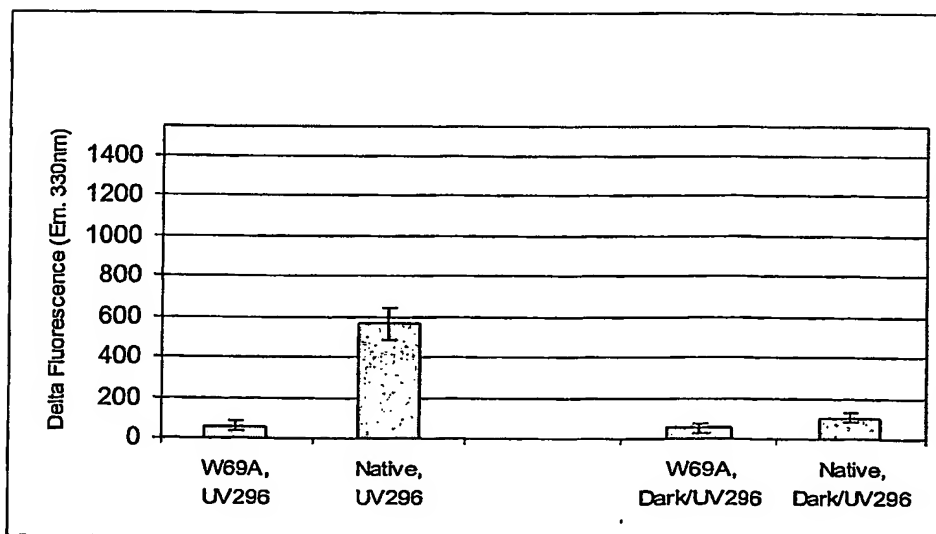
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Figure 13



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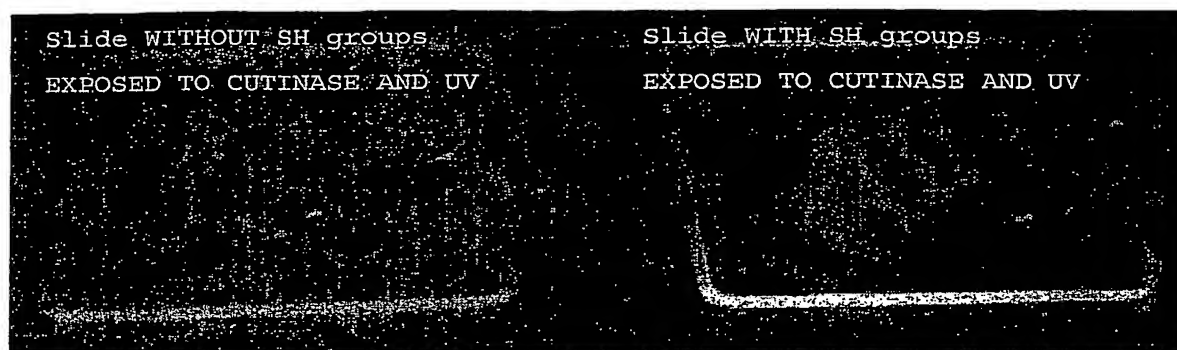
Figure 14

**A****B**



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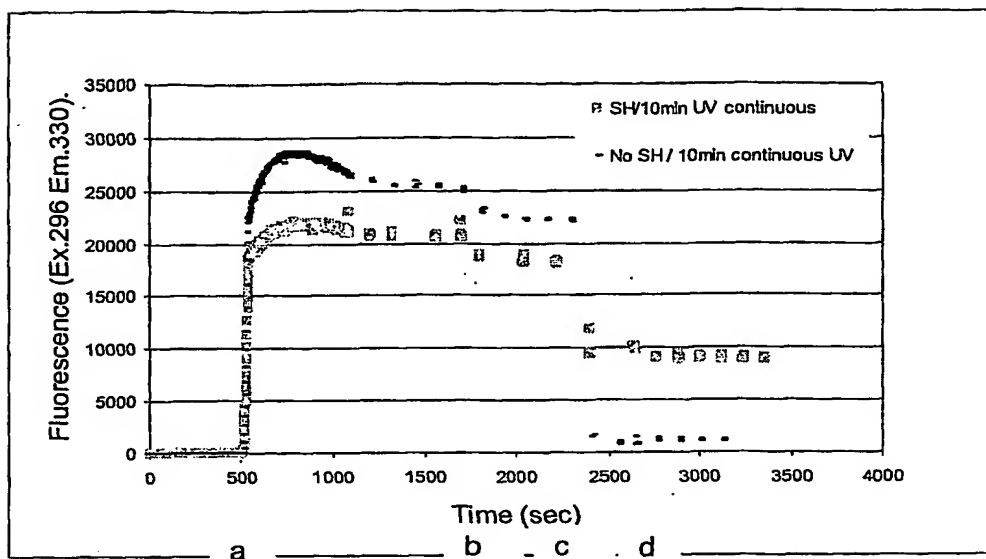
Figure 15



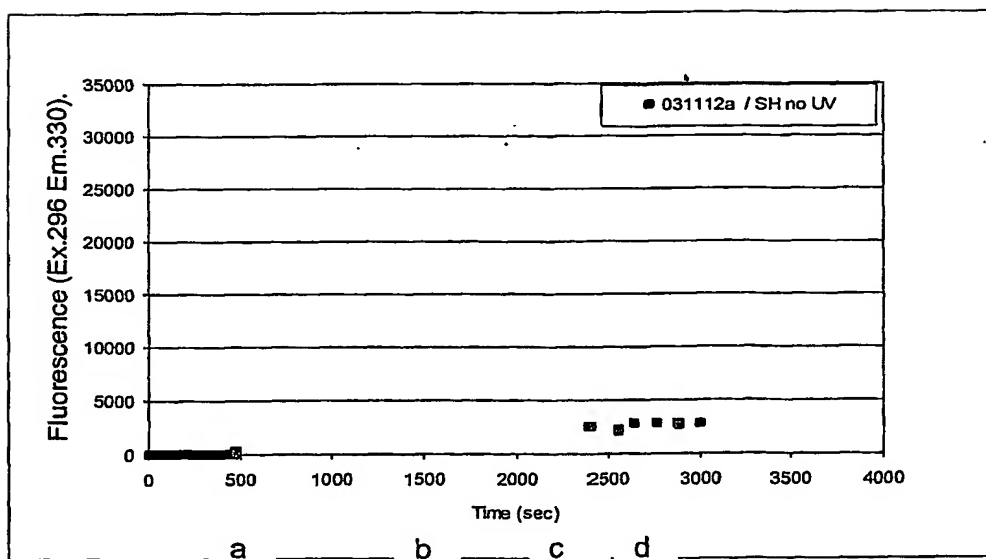
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Figure 16

A

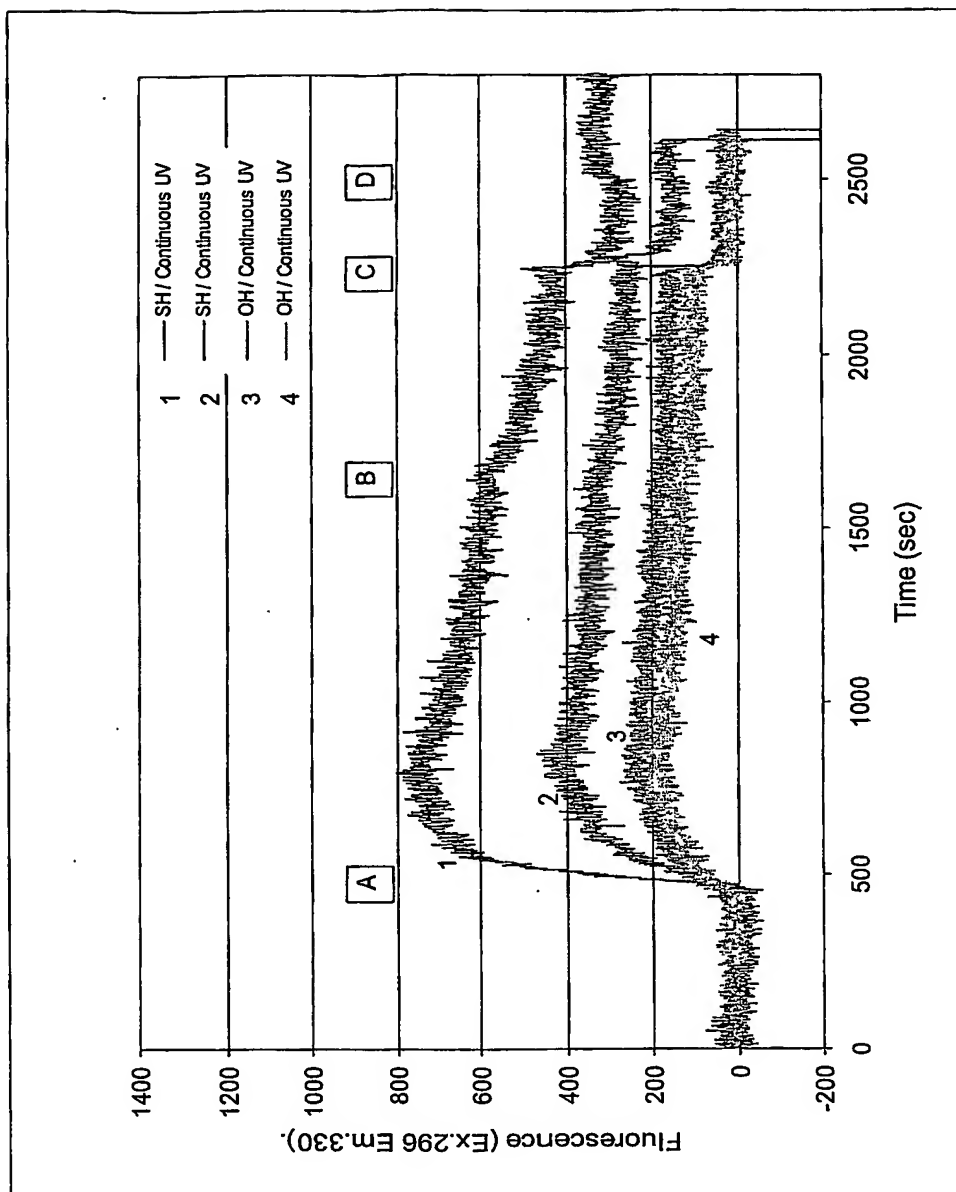


B



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C



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Figure 17 A

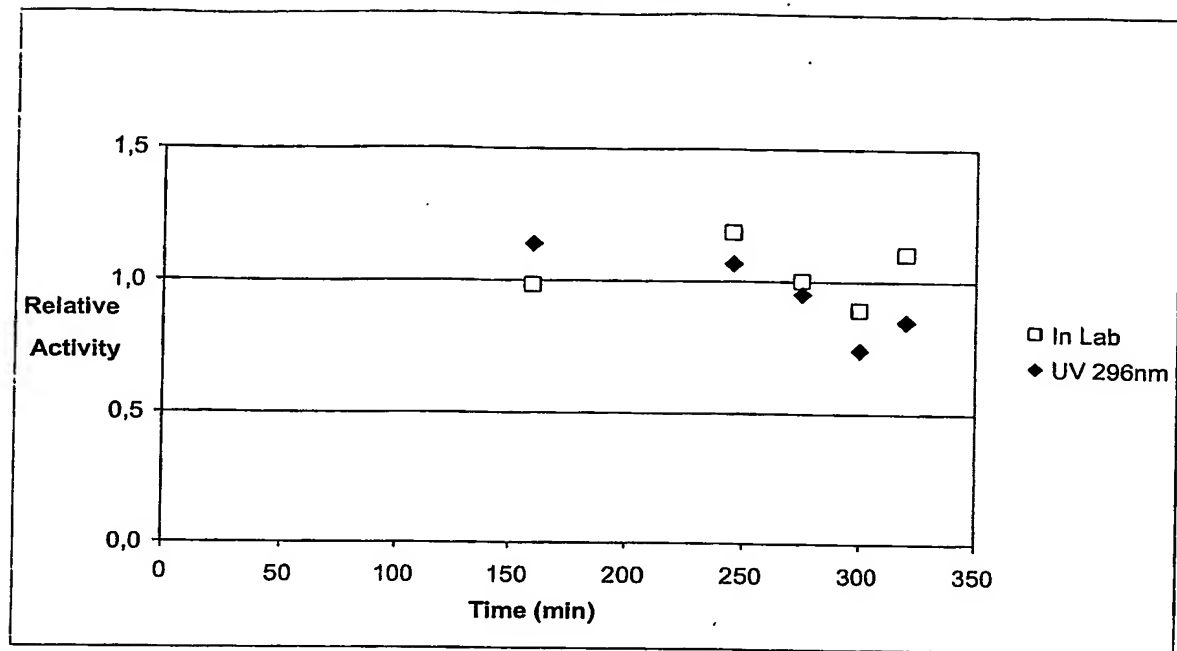


Figure 17B

